

SEQUENCE LISTING

<110> COSSON, BERTRAND
 PAILLARD, LUC
 LEGAGNEUX, VINCENT
 OSBORNE, HOWARD

<120> PEPTIDE PROTEIN TRANSLATION INHIBITOR AND THE USE
 THEREOF FOR PROTEIN TRANSLATION CONTROL

<130> 0510-1133

<140> 10/565,438

<141> 2006-01-20

<150> PCT/FR04/050345

<151> 2004-07-20

<160> 17

<170> PatentIn Ver. 3.3

<210> 1

<211> 28

<212> PRT

<213> *Xenopus laevis*

<400> 1

Val	Lys	Phe	Ala	Asp	Thr	Gln	Lys	Asp	Lys	Glu	Gln	Lys	Arg	Met	Thr
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Gln	Gln	Leu	Gln	Gln	Gln	Met	Gln	Gln	Leu	Asn	Ala
		20						25			

<210> 2

<211> 28

<212> PRT

<213> *Homo sapiens*

<400> 2

Val	Lys	Phe	Ala	Asp	Thr	Gln	Lys	Asp	Lys	Glu	Gln	Lys	Arg	Met	Ala
1				5					10					15	

Gln	Gln	Leu	Gln	Gln	Gln	Met	Gln	Gln	Ile	Ser	Ala
		20						25			

<210> 3

<211> 84

<212> PRT

<213> *Xenopus laevis*

<400> 3

Phe	Thr	Thr	Arg	Ser	Met	Ala	Gln	Met	Ala	Ile	Lys	Ser	Met	His	Gln
1				5					10					15	

Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Ile Val Val Lys Phe Ala
 20 25 30
 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln
 35 40 45
 Gln Gln Met Gln Gln Leu Asn Ala Ala Ser Met Trp Gly Asn Leu Thr
 50 55 60
 Gly Leu Asn Ser Leu Ala Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr
 65 70 75 80
 Ala Ser Ser Gly

<210> 4
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 4
 Phe Thr Thr Arg Ala Met Ala Gln Thr Ala Ile Lys Ala Met His Gln
 1 5 10 15
 Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Met Val Val Lys Phe Ala
 20 25 30
 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Ala Gln Gln Leu Gln
 35 40 45
 Gln Gln Met Gln Gln Ile Ser Ala Ala Ser Val Trp Gly Asn Leu Ala
 50 55 60
 Gly Leu Asn Thr Leu Gly Pro Gln Tyr Leu Ala Leu Tyr Leu Gln Leu
 65 70 75 80
 Leu Gln Gln Thr Ala Ser Ser Gly
 85

<210> 5
 <211> 189
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 fusion protein

<400> 5
 Met Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Val Lys Phe Ala
 1 5 10 15
 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln
 20 25 30

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<210> 6
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      fusion protein
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<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic fusion protein

Met 1	Ala	Ser	Asn	Phe 5	Thr	Gln	Phe	Val	Leu 10	Val	Asp	Asn	Gly	Gly 15	Thr
Gly	Asp	Val	Thr 20	Val	Ala	Pro	Ser	Asn 25	Phe	Ala	Asn	Gly	Val 30	Ala	Glu
Trp	Ile	Ser 35	Ser	Asn	Ser	Arg	Ser 40	Gln	Ala	Tyr	Lys	Val 45	Thr	Cys	Ser
Val	Arg 50	Gln	Ser	Ser	Ala	Gln 55	Asn	Arg	Lys	Tyr	Thr 60	Ile	Lys	Val	Glu
Val 65	Pro	Lys	Val	Ala	Thr 70	Gln	Thr	Val	Gly	Gly 75	Glu	Glu	Leu	Pro	Val 80
Ala	Gly	Trp	Arg	Ser 85	Tyr	Leu	Asn	Met	Glu 90	Leu	Thr	Ile	Pro	Ile 95	Phe

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr Gly Gly Gly Gly Gly Ser Lys Leu Gly Ser Met Ala Tyr Pro
 130 135 140

Tyr Asp Val Pro Asp Tyr Ala Arg Ala Ala
 145 150

<210> 7
 <211> 570
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 fusion polynucleotide

<400> 7
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 gcggccgcca tggcttctaa ctttactcag ttcggttctcg tcgacaatgg cggaactggc 180
 gacgtgactg tcgccccaaag caacttcgct aacgggggtcg ctgaatggat cagctctaac 240
 tcgcgatcac aggccttaca agtaacctgt agcggttcgct agagctctgc gcagaatcgc 300
 aaatacacca tcaaagtcga ggtgcctaaa gtggcaaccc agactggttg tgggaagag 360
 cttcctgtag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420
 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480
 ccgattccct cggccatcgc ggccaactcc ggcatctacg gaggtggagg tggatctggg 540
 ccctattcta tagtgtcacc taaatgctag 570

<210> 8
 <211> 570
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 fusion polynucleotide

<400> 8
 atggcttacc catacgatgt tccagattac gctagcgtaa aatttgctga tacacagaag 60
 gacaaagaac agaagagaat ggcccagcag ctcagcagc agatgcagca aatcagcgca 120
 gcggccgcca tggcttctaa ctttactcag ttcggttctcg tcgacaatgg cggaactggc 180
 gacgtgactg tcgccccaaag caacttcgct aacgggggtcg ctgaatggat cagctctaac 240
 tcgcgatcac aggccttaca agtaacctgt agcggttcgct agagctctgc gcagaatcgc 300
 aaatacacca tcaaagtcga ggtgcctaaa gtggcaaccc agactggttg tgggaagag 360
 cttcctgtag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420
 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480
 ccgattccct cggccatcgc ggccaactcc ggcatctacg gaggtggagg tggatctggg 540
 ccctattcta tagtgtcacc taaatgctag 570

<210> 9

<211> 489

<212> PRT

<213> *Xenopus laevis*

<400> 9

Met	Asn	Gly	Thr	Met	Asp	His	Pro	Asp	His	Pro	Asp	Pro	Asp	Ser	Ile	1	5	10	15
Lys	Met	Phe	Val	Gly	Gln	Val	Pro	Arg	Ser	Trp	Ser	Glu	Lys	Glu	Leu	20	25	30	
Arg	Glu	Leu	Phe	Glu	Gln	Tyr	Gly	Ala	Val	Tyr	Glu	Ile	Asn	Val	Leu	35	40	45	
Arg	Asp	Arg	Ser	Gln	Asn	Pro	Pro	Gln	Ser	Lys	Gly	Cys	Cys	Phe	Ile	50	55	60	
Thr	Phe	Tyr	Thr	Arg	Lys	Ala	Ala	Leu	Glu	Ala	Gln	Asn	Ala	Leu	His	65	70	75	80
Asn	Met	Lys	Val	Leu	Pro	Gly	Met	His	His	Pro	Ile	Gln	Met	Lys	Pro	85	90	95	
Ala	Asp	Ser	Glu	Lys	Asn	Asn	Ala	Val	Glu	Asp	Arg	Lys	Leu	Phe	Ile	100	105	110	
Gly	Met	Val	Ser	Lys	Asn	Cys	Asn	Glu	Asn	Asp	Ile	Arg	Ala	Met	Phe	115	120	125	
Ser	Pro	Phe	Gly	Gln	Ile	Glu	Glu	Cys	Arg	Ile	Leu	Arg	Gly	Pro	Asp	130	135	140	
Gly	Met	Ser	Arg	Gly	Cys	Ala	Phe	Val	Thr	Phe	Thr	Thr	Arg	Ser	Met	145	150	155	160
Ala	Gln	Met	Ala	Ile	Lys	Ser	Met	His	Gln	Ala	Gln	Thr	Met	Glu	Gly	165	170	175	
Cys	Ser	Ser	Pro	Ile	Val	Val	Lys	Phe	Ala	Asp	Thr	Gln	Lys	Asp	Lys	180	185	190	
Glu	Gln	Lys	Arg	Met	Thr	Gln	Gln	Leu	Gln	Gln	Gln	Met	Gln	Gln	Leu	195	200	205	
Asn	Ala	Ala	Ser	Met	Trp	Gly	Asn	Leu	Thr	Gly	Leu	Asn	Ser	Leu	Ala	210	215	220	
Pro	Gln	Tyr	Leu	Ala	Leu	Leu	Gln	Gln	Thr	Ala	Ser	Ser	Gly	Asn	Leu	225	230	235	240
Asn	Ser	Leu	Ser	Gly	Leu	His	Pro	Met	Gly	Ala	Glu	Tyr	Gly	Thr	Gly	245	250	255	
Met	Thr	Ser	Gly	Leu	Asn	Ala	Ile	Gln	Leu	Gln	Asn	Leu	Ala	Ala	Leu	260	265	270	

Ala Ala Ala Ala Ser Ala Ala Gln Asn Thr Pro Ser Ala Gly Ala Ala
 275 280 285
 Leu Thr Ser Ser Ser Ser Pro Leu Ser Ile Leu Thr Ser Ser Gly Ser
 290 295 300
 Ser Pro Ser Ser Asn Asn Ser Ser Ile Asn Thr Met Ala Ser Leu Gly
 305 310 315 320
 Ala Leu Gln Thr Leu Ala Gly Ala Thr Ala Gly Leu Asn Val Asn Ser
 325 330 335
 Leu Ala Gly Met Ala Ala Phe Asn Gly Gly Leu Gly Ser Ser Leu Ser
 340 345 350
 Asn Gly Thr Gly Ser Thr Met Glu Ala Leu Ser Gln Ala Tyr Ser Gly
 355 360 365
 Ile Gln Gln Tyr Ala Ala Ala Ala Leu Pro Ser Leu Tyr Asn Gln Ser
 370 375 380
 Leu Leu Ser Gln Gln Gly Leu Gly Ala Ala Gly Ser Gln Lys Glu Gly
 385 390 395 400
 Pro Glu Gly Ala Asn Leu Phe Ile Tyr His Leu Pro Gln Glu Phe Gly
 405 410 415
 Asp Gln Asp Leu Leu Gln Met Phe Met Pro Phe Gly Asn Val Val Ser
 420 425 430
 Ser Lys Val Phe Ile Asp Lys Gln Thr Asn Leu Ser Lys Cys Phe Gly
 435 440 445
 Phe Val Ser Tyr Asp Asn Pro Val Ser Ala Gln Ala Ala Ile Gln Ser
 450 455 460
 Met Asn Gly Phe Gln Ile Gly Met Lys Arg Leu Lys Val Gln Leu Lys
 465 470 475 480
 Arg Ser Lys Asn Asp Ser Lys Pro Tyr
 485

<210> 10

<211> 1470

<212> DNA

<213> *Xenopus laevis*

<400> 10

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 gccgtctatg aaattaatgt tctccgagac agaagccaga atcctcctca gagcaaagga 180
 tgctgtttta ttactttcta cacaagaaaa gctgcgttag aagcacagaa tgctttgcac 240
 aacatgaaag ttctccctgg gatgcatcat ccaatacaga tgaagccagc cgacagtga 300
 aagaataatg ctgtggaaga ccgaaagcta tttatcggaa tggtttccaa gaattgta 360
 gagaatgata tccgggccat gttctctccg tttggacaga tagagggaatg tcgtatcctg 420
 cgaggccctg atggaatgag cagaggatgt gcattcggtta cgtttacaac tagatccatg 480
 gcacagatgg caatcaaadc catgcaccaa gcacaaacca tggagggtg ttcctcacca 540

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atagtggtaa agttcgcaga cactcagaaa gacaaagaac agaagcgcac gacgcagcaa 600
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aacagcttgg caccocagta tttagcactc ctccagcaga ccgcctcctc tgggaacctc 720
aactccctaa gtggtctcca ccctatggga gctgagtacg gcaactggaat gacatcaggg 780
cttaatgcca tacagttaca gaatttggca gctttagcgg ctgctgctag tgctgcgcag 840
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agttccgggt cctccccagc ttcaaataac tcatccatca acaccatggc atccctagga 960
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gcccttagtc aagcttactc tgggattcag cagtatgctg ccgctgcact tccttcactc 1140
tataaccaga gccttttgtc acaacagggt ttgggggctg cggggagtc gaaagaaggc 1200
ccagaaggag ccaacctttt tatataccac ctaccccagg agtttgggga ccaggatctc 1260
ctgcagatgt tcatgccatt tggaaatggt gtgtcctcca aagttttcat cgacaaacaa 1320
acgaacctca gcaaattgtt tggcttcgta agttacgaca atcccgtttc tgctcagggt 1380
gctatccagt ccatgaacgg ctttcagatc ggaatgaaac gcctgaaagt ccaactcaaa 1440
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<210> 11

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 11

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1

5

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12

atgctagcgt aaagttcgca gacactcaga aag

33

<210> 13

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13

atgcggccgc tgcattgagc tgctgcattt gc

32

<210> 14
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 14
 atgctagcgt aaaatttgct gatacacaga ag 32

<210> 15
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 15
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<210> 16
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 16
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<210> 17
 <211> 10
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 poly-A tail

<400> 17
 aaaaaaaaaa 10